

## REMARKS

The changes to the specification resulting from the above amendments are shown in attached Appendix A.

Applicants have amended the specification to identify the sequences in the present application by a SEQ. ID. No. In addition, applicants have submitted paper and machine readable versions of the sequence listing together with a Statement in Accordance with 37 CFR §1.821(g).

Respectfully submitted,

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I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: U.S. Patent and Trademark Office, P.O. Box 2327, Arlington, VA 22202	
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## Appendix A

### Version of Amended Claims With Markings to Show Changes Made

In reference to the amendments made herein to the specification, additions appear as double underlined text, while deletions appear as bracketed text, as indicated below:

In the Specification:

#### At page 72, lines 18:

G6PDEx6-3L5' CAC GCT ATC CCG TTA GAC ATT GTC AAG CAG GCG ATG TTG TCC CGG TTC 3'  
(SEQ. ID. NO. 1)  
G6PDEx6-4R5' CAG ATG GGG CCG AAG ATC CTG TTA TTG ATA CAT AGT GCG GTA GTT GGC 3'  
(SEQ. ID. NO. 2)  
erbBEx1-5L 5' CAC GCT ATC CCG TTA GAC ATC GCC CTG ATG GGG AGA ATG TGA AAA TTC 3'  
(SEQ. ID. NO. 3)  
erbBEx1-6R 5' CAG TGG CCA TCA AAG TGT TGA GGG AGC GTA CAT AGT GCG GTA GTT GGC 3'  
(SEQ. ID. NO. 4)  
Int2Ex3-7L 5' CAC GCT ATC CCG TTA GAC ATT CAT AAC CCT TGC CGT TCA CAG ACA CGT AC 3'  
(SEQ. ID. NO. 5)  
Int2Ex3-8R 5' CAC AGT CTC TCG GCG CTG GGC AAT AAT ACA TAG TGC GGT AGT TGG C 3' (SEQ. ID. NO. 6)  
p53Ex8-9L 5' CAC GCT ATC CCG TTA GAC ATC TTA GTA ATT GAG GTG CGT GTT TGT GCC TGT C 3' (SEQ. ID. NO. 7)  
p53Ex8-10R 5' CTG GGA GAG ACC GGC GCA CAT TAC TAC ATA GTG CGG TAG TTG GC 3' (SEQ. ID. NO. 8)  
SODEx-3-11L 5' CAC GCT ATC CCG TTA GAC ATC TGT ACC AGT GCA GGT CCT CAC TTT AAT C 3' (SEQ. ID. NO. 9)  
SODEx-3-12R 5' CTC TAT CCA GAA AAC ACG GTG GGC CGC TAC ATA GTG CGG TAG TTG GC 3' (SEQ. ID. NO. 10)

#### PCR Primers:

ZipALg1F 5' Fam-GGA GCA CGC TAT CCC GTT AGA C 3' (SEQ. ID. NO. 11) (Tm = 71°C)  
ZipBLg2R 5' CGC TGC CAA CTA CCG CAC TAT G 3' (SEQ. ID. NO. 12) (Tm = 72°C)

(Underlined sequences are common between LDR probes and ZipALg1F or the complement of ZipBLg2R.)

At page 84, Table 9:

Table 9 - LDR Oligonucleotide Sequences

Locus	Allele-Specific Oligonucleotide (5'-->3')	Common Oligonucleotide (5'-->3')
1	FAM-AGCTTCAATGATGAGAACCTGC (SEQ. ID. NO. 13) TET-AGCTTCAATGATGAGAACCTGT (SEQ. ID. NO. 15)	P-GCATAGTGGTGGCTGACCTGTTTCATAT (SEQ. ID. NO. 14)
2	FAM-CTCCATGGGCCAGCC (SEQ. ID. NO. 16) TET-CTCCATGGGCCAGCT (SEQ. ID. NO. 18)	P-AGCACTGGTGGCCTGTGAG (SEQ. ID. NO. 17)
3	FAM-GGGGACAGCCATGCACTGA (SEQ. ID. NO. 19) TET-GGGGACAGCCATGCACTGC (SEQ. ID. NO. 21)	P-GCCTCTGGTAGCCTTTCAACCATA (SEQ. ID. NO. 20)
4	FAMTTAGAAATCATCAAGCCTAGGTCAT (SEQ. ID. NO. 22) TET-TTAGAAATCATCAAGCCTAGGTCAG (SEQ. ID. NO. 24)	P-CACCTTTTAGCTTCTGAGCAATGAT (SEQ. ID. NO. 23)
5	HEX-GGTTGTATTGTGACCATATTAATTA (SEQ. ID. NO. 25) HEX-ATGGTTGTATTGTGACCATATTAATTG (SEQ. ID. NO. 27)	P-ATTTTCTCTATTGTTTCATCTTTCAGGA (SEQ. ID. NO. 26)
6	FAM-GGGCCAAGAAGGTATCTACCA (SEQ. ID. NO. 28) TET-GGGCCAAGAAGGTATCTACCG (SEQ. ID. NO. 30)	P-ATAGTGTCTATTAGGCATTGAAAAATGTGTAT (SEQ. ID. NO. 29)
7	FAM-ACACAGCAGCTTACTCCAGAGG (SEQ. ID. NO. 31) TET-ACACAGCAGCTTACTCCAGAGA (SEQ. ID. NO. 33)	P-TCAAGTCCAAGGCCATTGGCTTATA (SEQ. ID. NO. 32)
8	FAM-CCAGCAAAGAGAAAAGAAGGG (SEQ. ID. NO. 34) TET-CCAGCAAAGAGAAAAGAAGGA (SEQ. ID. NO. 36)	P-CCCCAGAAATCACAGGTGGGCTAT (SEQ. ID. NO. 35)
9	FAM-ATGATATTAGAGCTCACTCATGTCCA (SEQ. ID. NO. 37) TET-ATGATATTAGAGCTCACTCATGTCCG (SEQ. ID. NO. 39)	P-TCAGTTTGAAAAAGACAAAGAATTCTTT (SEQ. ID. NO. 38)
10	HEX-TGCTGTCTTCCAGGAATCTGTT (SEQ. ID. NO. 40) HEX-ATTGCTGTCTTCCAGGAATCTGTG (SEQ. ID. NO. 42)	P-CAACTCTCTCGAAGCCATGTTACAA (SEQ. ID. NO. 41)
11	HEX-GGACATAGTGACCGTGCAGGTC (SEQ. ID. NO. 43)	P-CTTCCCCAGTGTGAGTGCCGTA (SEQ. ID. NO. 44)

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HEX-ATGGACATAGTGACCGTGCAGGTT  
(SEQ. ID. NO. 45)

12 HEX-CTATGACACCGTCATCAGCAGG (SEQ. ID. NO. 46) P-GACATCCAGGCCCCCGAC (SEQ. ID. NO. 47)

HEX-TACTATGACACCGTCATCAGCAGA (SEQ. ID. NO. 48)

The allele-specific oligonucleotides are 5' end labeled with either FAM, TET, or HEX. All the common oligonucleotides are phosphorylated at the 5' end. Underline denotes tails that are not complementary to the target sequence. LDR primer sets were designed in two ways: (i) allele-specific primers were of the same length but contained either FAM or TET label; or (ii) the allele-specific primers were both labeled with HEX but differed in length by two bases.

At page 88-89, Table 11:

TABLE 11 - Primary PCR Primer Sequences

Number or Name	Primer (5'→3')
1	F <u>GGAGCACGCTATCCCGTTAGACAGCCAAGGGGAACCCTGAGAG</u> (SEQ. ID. NO. 49) R <u>CGCTGCCAACTACCGCACTATGATCGTGGTCGAGGTGGTCACCATC</u> (SEQ. ID. NO. 50)
2	F <u>CCTCGTTGCGAGGCGTATTCTGTATTTCCTCTTCTGTAAAAGGGAAGTTTGT</u> (SEQ. ID. NO. 51) R <u>GCGACCTGACTTGCCGAAGAACAATGTCCCATCTCCTCTACCTGATAC</u> (SEQ. ID. NO. 52)
3	F <u>GGAGCACGCTATCCCGTTAGACTAAAGATCTGTCTTGCGTCCCAGTCA</u> (SEQ. ID. NO. 53) R <u>CGCTGCCAACTACCGCACTATGTATCAATTTTGCAGAGCTTAGATGGAATG</u> (SEQ. ID. NO. 54)
4	F <u>CCTCGTTGCGAGGCGTATTCTGTAGCACTTGTGATCATGGTTTTAGAAATC</u> (SEQ. ID. NO. 55) R <u>GCGACCTGACTTGCCGAAGAACAATATCGTATTGATGATCCTCATAAAGTTG</u> (SEQ. ID. NO. 56)
5	F <u>GGAGCACGCTATCCCGTTAGACATCAGCCACTTGGAAGGAGCAAAC</u> (SEQ. ID. NO. 57) R <u>CGCTGCCAACTACCGCACTATGATGGACCATGGCTGAGTCTCCTTTAG</u> (SEQ. ID. NO. 58)
6	F <u>CCTCGTTGCGAGGCGTATTCTGAACCAACACGGAGAAGCATTGTTTTTC</u> (SEQ. ID. NO. 59) R <u>GCGACCTGACTTGCCGAAGAACAATTAGCCTCAATCCTCATACTGACCTCTAC</u> (SEQ. ID. NO. 60)

- 7 F GGAGCACGCTATCCCGTTAGACATCTCCTAACATCTATGTACTGGATTATCTAAATG  
(SEQ. ID. NO. 61)  
R CGCTGCCAACTACCGCACTATGATCTTACTCAAGTAATCACTCACCAGTGTTG (SEQ.  
ID. NO. 62)
- 8 F CCTCGTTGCGAGGCGTATTCTGAATGAGTCAAATTGGCCTGGACTTG (SEQ. ID. NO.  
63)  
R GCGACCTGACTTGCCGAAGAAC**TTAATTCCCGTGAGAAGGGAGATG** (SEQ. ID. NO.  
64)
- 9 F CCTCGTTGCGAGGCGTATTCTGAAGGATCTGGATGAAGCCATTCTAAAC (SEQ. ID.  
NO. 65)  
R GCGACCTGACTTGCCGAAGAAC**TTGAAAAGGTATTATAAGCAGAGAAAAGATG**  
(SEQ. ID. NO. 66)
- 10 F GGAGCACGCTATCCCGTTAGACAGGACCGCAAAAGGCTTTTCATC (SEQ. ID. NO. 67)  
R CGCTGCCAACTACCGCACTATGTAGCACCCAGGCTGTACCCAATTAG (SEQ. ID. NO.  
68)
- 11 F CCTCGTTGCGAGGCGTATTCTGATCGGGCGCTGGGCTTCAC (SEQ. ID. NO. 69)  
R GCGACCTGACTTGCCGAAGAACATCAGATGCCGCACTCCAAGAAG (SEQ. ID. NO.  
70)
- 12 F GGAGCACGCTATCCCGTTAGACATAAGAGCCCACGGCGTCTCTTC (SEQ. ID. NO. 71)  
R CGCTGCCAACTACCGCACTATGTAAGAGACAGTGCCCAGGACAGAGTC (SEQ. ID.  
NO. 72)
- ZipALg1 F GGAGCACGCTATCCCGTTAGAC (SEQ. ID. NO. 73)  
ZipBLg2 R CGCTGCCAACTACCGCACAT G (SEQ. ID. NO. 74)  
ZipCLg3 F CCTCGT GCGAGGCGTATTCT G (SEQ. ID. NO. 75)  
ZipDLg4 R GCGACCTGACTTGCCGAAGAAC (SEQ. ID. NO. 76)

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Solid underline denotes the ZipALg1 and ZipBLg2 sequences. Dotted underline denotes the ZipCLg1 and ZipDLg2 sequences. Linker sequences are indicated in bold. F=forward, R=reverse

Table 9 - LDR Oligonucleotide Sequences

Locus	Allele-Specific Oligonucleotide (5'-->3')	Common Oligonucleotide (5'-->3')
1	FAM-AGCTTCAATGATGAGAACCTGC TET-AGCTTCAATGATGAGAACCTGT	P-GCCTAGTGGTGGCTGACCTGTT <u>CATAT</u>
2	FAM-CTCCATGGGCCCAGCC TET-CTCCATGGGCCCAGCT	P-AGCACTGGTGGCCCTGTGAG
3	FAM-GGGGACAGCCATGCACTGA TET-GGGGACAGCCATGCACTGC	P-GCCTCTGGTAGCCTTTCAACCATA
4	FAMTTAGAAATCATCAAGCCTAGGTCAT TET-TTAGAAATCATCAAGCCTAGGTCAG	P-CACCTTTTAGCTTCCTGAGCAATG <u>AT</u>
5	HEX-GGTTGTATTGTGCACCATATTAATTA HEX- <u>AT</u> GGTTGTATTGTGCACCATATTAATTG	P-ATTTTCTCTATTGTTTTCATCTTTCAGGA
6	FAM-GGGCCAAGAAGGTATCTACCA TET-GGGCCAAGAAGGTATCTACCG	P-ATAGTGTCTATTAGGCATTGAAAATGTG <u>TAT</u>
7	FAM-ACACAGCAGCTTACTCCAGAGG TET-ACACAGCAGCTTACTCCAGAGA	P-TCAAGTCCAAGGCCATTGGCTT <u>ATA</u>
8	FAM-CCAGCAAAGAGAAAAGAAGGG TET-CCAGCAAAGAGAAAAGAAGGA	P-CCCCAGAAATCACAGGTGGGCT <u>AT</u>
9	FAM-ATGATATTAGAGCTCACTCATGTCCA TET-ATGATATTAGAGCTCACTCATGTCCG	P-TCAGTTTGAAAAAGACAAAGAATTCTTT
10	HEX-TGCTGTCTTCCAGGAATCTGTT HEX- <u>ATT</u> GCTGTCTTCCAGGAATCTGTG	P-CAACTCTCTCGAAGCCATGTTCA <u>CAA</u>
11	HEX-GGACATAGTGACCGTGCAGGTC HEX- <u>AT</u> GGACATAGTGACCGTGCAGGTT	P-CTTCCCCAGTGTGAGTGCCG <u>TA</u>
12	HEX-CTATGACACCGTCATCAGCAGG HEX-TACTATGACACCGTCATCAGCAGA	P-GACATCCAGGCCCCCGAC

The allele-specific oligonucleotides are 5' end labeled with either FAM, TET, or HEX. All the common oligonucleotides are phosphorylated at the 5' end. Underline denotes tails that are not complementary to the target sequence. LDR primer sets were designed in two ways: (i) allele-specific primers were of the same length but contained either FAM or TET label; or (ii) the allele-specific primers were both labeled with HEX but differed in length by two bases.